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1	15 16	30 31	45 46	60 61	75 76	90
1 mtblder	MNEI.VD TTENYLRTI	YOLEEEGV TPLRARI	AERLDOSGPTVSQT V	SNHERDGLLRVAGDR	HLELTNGRALAI AV	MRKHRLAERLLLV DVI
2 dtxr	MKDLVDTTENYLRTI	YELEEGSV TPLRARI	AERLEQSGPTVSOT V	ARNERDGLVVVASD-	SLOHTPTGRTLAT AV	MRKHRLAERLLLT DII
3 staphelislr	-----	---HTVSCPPPS--T	SRESEQ-----ARAL	CLRLLTARSRTRAEL	AGQLAKRCYPEDIGN	RVLDRLA AVGLVDDT
1	105 106	120 121	135 136	150 151	165 166	180
1 mtblder	GLPWEEVHAEACRWE	HVMSEDEVERRLVKVL	NNPTTSPFGNPIGL	VELGVPEPGADDAN	LVRLTLPAGSPVAV	VVRQLTEHVQGGIDL
2 dtxr	GILDINKVHDEACRWE	HVMSEDEVERRLVKVK	DVSR-SPFGNPIGL	DELGVGNS--DAAAP	GTRVIDAATSMPK V	RIVOGNEIFQVETDQ
3 staphelislr	DFAEQHVQSRANAA	KSKRALAAELIHA KV	DDDVITTVLGIDAG	AERGRAECK--LVRAR	LRREVLIDDGTD EAR	VSRRLVNLARRG-Y
1	195 196	210 211	225 226	240 241	255 256	270
1 mtblder	ITRLKADGVVPNAR V	TVETTPCGGV TIVIP	GHENVTLPHENAHAV	KVEKV	230	
2 dtxr	FOLLADADIRVGSEVE	IVDRD--GHITLSHN	GKD-VELLDLAIHTI	RIEEL	223	
3 staphesislr	GOT'LACEVVIJAE LAA	ERERR--RV-----	-----	174		

FIGURE 1

1	15	16	30	31	45	46	60	61	75	76	90	
1 MI.	MNDLVDTENTYLRTI	YOLEEEGIVTPIBAR	IAER-----	PTVSOT	VSRMERDGLRYAGN	RHIELTTKGRAMAIA	VMKKNRLAERLLVDV					85
2 TB	MNELVDTEENTYLRTI	YOLEEEG--VTPIBAR	IAERYDOOSGTSVST	VSARMEDDGLRYAGD	RHIELTEKGRALATA	VMKKNRLAERLLVDV						89
3 MS	MNDLVDTENTYLRTI	YOLEEEG-VVPIBAR	IAERLDOSGTSVST	VSARMEDDGLRYAGD	RHIELTEKGRALATA	VMKKNRLAERLLVDV						89
4 MCB	MVSCSPRSTSER---	---EEQARALCYRL	TARS-----	RTARL	ACOLAKRGYFEDIGN	RULD-----	RLAANG	LVDOTDFAEQ-----				70
1 MI.	91	105	106	120	121	135	136	150	151	165	166	180
1 MI.	IGAPMEEVNAEACSM	ENHVSSEDEVERLLKV	LNPPTSPGPNPIG	LLDLGAPDASAANA	KLVRLTELPSSPVA	VVVRLQLTENVD-DID						174
2 TB	IGAPMEEVNAEACSM	ENHVSSEDEVERLLKV	LNPPTSPGPNPIG	LVELSGEREGADA	NLVRLTELPASPVA	VVVRLQLTENVOGDI						179
3 MS	IGAPMEEVNAEACSM	ENHVSSEDEVERLLKV	LENPTSPGPNPIG	LTLEAVTPGVNTEVD	SLVRLTELPQHPVA	VVVRLQLTENVOGDT						179
4 MCB	-----WVQS--RANA	KSRIKALAEELNAKV	DDVDTTVLGC-IDA	GAERGR--AEKLVA	RLAREVLIDDOCTDEA	RVSRLVAMLA-----						148
1 MI.	101	195	196	210	211	225	226	240	241	255	256	270
1 MI.	LITRLKQOTGVENBAR	VTVETSPAGNVITII	PGHENVTLPHEMANA	VAVEKV---								225
2 TB	LITRLKQAGVENBAR	VTVETTPGGCVITII	PGHENVTLPHEMANA	VAVEKV---								230
3 MS	LIGRLKEAGVENBAR	VTVEANNGGVNITVI	PGHEDELPRHMANA	VAVEKEKV								233
4 MCB	-----RGTGQTLACEV	VIAELAEERERARV-	-----									174

FIGURE 2

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	10	20	30	40	50	60	
B1 DtxR		MKDLVDTTEM	YLRTIYELEE	EGIVPLRARI	AERLEQSGPT	VSQTVARMER	DGLVHVSPDR
Cd DtxR		MKDLVDTTEM	YLRTIYELEE	EGVTPLRARI	AERLEQSGPT	VSQTVARMER	DGLVVVASDR
Mt IdeR		MNELVDTTEM	YLRTIYDLEE	EGVTPLRARI	AERLDQSGPT	VSQTVSRMER	DGLLRVAGDR
Ms IdeR		MNDLVDTTEM	YLRTIYDLEE	EGVVPRLARI	AERLDQSGPT	VSQTVSRMER	DGLLRVAGDR
Ml IdeR		MNDLVDTTEM	YLRTIYDLEE	EGIVTPLRARI	AER PT	VSQTVSRMER	DGLLRVAGNR
Sl DesR		MSGLIDTTEM	YLRTILELEE	EGVVPMRARI	AERLDQSGPT	VSQTVARMER	DGLVSVAADR
Se SirR	M	LTEEKED	YLKAILTNDG	DVSFVSNKKL	SQFLNIKPPS	VSEMVGRLK	EGYVETKHYK
Sa SirR	M	LTEEKED	YLKAILTNNG	DKNFVTNKIL	SQFLNIKPPS	VSEMVGRLK	AGYVETKPYK
Ef	M	TPNRED	YLKLIFELGG	DEVKVNKKQI	VSGLDVSAAS	VSEMISKLVK	EDLVEHSPYQ
Sg	M	TPNKED	YLKCLYELGT	RHNKITNKEI	AGLMQVSPPA	VTEMMKKLLA	EELLIKDKKA
Sm	M	TPNKED	YLKIIYELSE	RDEKISNKQI	AEKMSVSAPA	VSEMVKKLLL	EDLVLKDKQA
Spn	M	TPNKED	YLKCIYEIGI	DLHKITNKEI	AARMQVSPPA	VTEMIKRMKS	ENLILKKEC
Spy	M	TPNKED	YLKCIYEIGI	DLHKITNKEI	AARMQVSPPA	VTEMIKRMKS	ENLILKKEC
CONSENSUS		M--*-----E*	YL*-I*-----	-----NK-*	*-----P-	*****-----	*-L-----
		70	80	90	100	110	120
B1 DtxR		SLEMTPEGRS	LAIAMVRNDR	LAERLLTDII	GLDIHKVHDE	ACRWEHVMSD	EVERRLVEVL
Cd DtxR		SLQMTPTGRT	LATAVMRKHR	LAERLLTDII	GLDINKVHDE	ACRWEHVMSD	EVERRLVKVL
Mt IdeR		HLELTEKGRA	LAIAMVRKHR	LAERLLVDVI	GLPWEEVHAE	ACRWEHVMSD	DVERRLVKVL
Ms IdeR		HLELTDKGRA	LAVAMVRKHR	LAERLLVDVI	LPWEDGVHAE	ACRWEHVMSD	EVERRLVQVL
Ml IdeR		HLELTTKGRA	MAIAMVRKHR	LAERLLVDVI	GLPWEEVHAE	ACRWEHVMSD	DVERRLIKVL
Sl DesR		HLELTDGRR	LATRVMRKHR	LAERLLVDVI	GLEWEQVHAE	ACRWEHVMSD	AVERRVLELL
Se SirR		GARLTEEGLK	QTLDIKRRH	LLRLFLIEIL	QYNWEEVHAE	AEILEHRISD	LFVERLDKIL
Sa SirR		GVRITDGLT	HTLDII RHR	LLELFLIEIL	KYNWEEVHAE	AEILEHRISD	LFVERLDKIL
Ef		GVQLTEKGLK	KASTLIRKHR	IWEVFLVEHL	NYTWNDVHEE	AEVLEHVTSD	TLVNRLADYL
Sg		GYLLTDLGLK	LVSDLYRKHR	LIEVFLVHHL	GYTTEEIHEE	AEVLEHTVSD	HFVERLDQLL
Sm		GYLLTKKGQI	LASSLYRKHR	LIEVFLMNHL	NYTADEIHEE	AEVLEHTVSD	VFVERLDKFL
Spn		GYLLTDLGLK	LVSELYRKHR	LIEVFLVHHL	DYTSQDIHEE	AEVLEHTVSD	LFVERLDKLL
Spy		GYLLTDLGLK	LVSELYRKHR	LIEVFLVHHL	DYTSQDIHEE	AEVLEHTVSD	LFVERLDKLL
CONSENSUS		---LT-G--	-----**HR	L--*L---L	-----H-E	A--*EH-S*	---*R---L
		130	140	150	160	170	180
B1 DtxR		DDVHRSPFGN	PIPLGLGEIGL	DQADEPDSGV	RAIDLPLGEN	LKARIVQVNE	ILQVDLEQFQ
Cd DtxR		KDVSRSPFGN	PIPLGLDELGV	GNSDAAAPGT	RVIDAATSMP	RKVRIVQVNE	IFQVETDQFT
Mt IdeR		NNPTTSPFGN	PIPLGLVELGV	GPEPGADDAN	LVRLTELPAG	SPVAVVVRQL	TEHVQGDIDL
Ms IdeR		ENPTTSPFGN	PIPLGTELAV	TPGVNTEDVS	LVRLTELPVG	MPVAVVVRQL	TEHVQGDIDL
Ml IdeR		NNPTTSPFGN	PIPLGLDLGA	GPDAASANAK	LVRLTELPVG	SPVAVVVRQL	TEHV DDIDL
Sl DesR		RHPTESPYGN	PIPLGLEELGE	TDGADPFLDE	GMVSLADLDP	GOEGKTVVVR	RIGEPIDTDA
Se SirR		NFPKTCPHGG	VIP	R GNSDAAAPGT	SILNFEPGER	VTVRRV RDK	TELL
Sa SirR		NFPKTCPHGG	VIP	R NNEYKEYIT	TILNYPEGDI	VTIKRV RDK	TDLL
Ef		NHPEFCPHGG	VIPEDNQPIH	EEKROTLDY	PVGTKIRIAR	VLDEKELLDY	LVSIDLNIQE
Sg		DYPKACPHGG	TIPAKGELLV	EKHKLTLLEA	KEKGDYILAR	VHDNFDLLTY	LERNGLQVKG
Sm		NYPKVCPHGG	TIPGHGOPLV	ERYRTTLKGV	TEMGVYLLKR	VQDNFOLLKY	MEQHHLKIGD
Spn		GFPKTCPHGG	TIPAKGELLV	EINNPLADI	KEAGAYRLTR	VHDSFDILHY	LDKHSILHIGD
Spy		GFPKTCPHGG	TIPAKGELLV	EINNPLADI	KEAGAYRLTR	VHDSFDILHY	LDKHSILHIGD
CONSENSUS		--P--*P*G*	-IP-----*	-----	-----	-----	-----

FIGURE 3

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B1 DtxR 190 200 210 220 230
 Cd DtxR ALTDAGVEIG TEVDIINEQG RVVITHNGSS VELIDDLAHA VRVEKVEG
 Mt IdeR QLLDADIRVG SEVEIVDRDG HITLSHNGKD VELLDDLAHT IRIEEL
 Ms IdeR ITRLKDAGVV PNARVTVETT PGGGVTVIVIP GHENVTLPHH MAHAVKVEKV
 Ml IdeR IGRLKEAGVV PNARVTVEAN NNGGVMIVIP GHEQVELPHH MAHAVKKKVE KVEKV
 ITRLKDTGVV PNARVTVETS PAGNVIIIIP GHENVTLPHH MAHAVKVEKV

Sl DesR QLMYTLRRAG VQPGSVVSVT ESAGGVLVGS GGEAAELEAD TASHVFVAKR
 Sa SirR VYLSSKDIYI GNTVEIVSKD DTNKVIILKR NDIVTILSYE NAMNIFAEK
 Sa SirR IYLSSKDISI GNEVEIVSKD EMNKVIIIKR NDNVIVSYE NAMNMFAEK
 Ef EYTIKEIAAY EGPITIYNEN KELSVSFKAA NTIFVEPLIR ESEEN
 Sg SgoR TIRFLGYDDF SHLYSLEVDG QEIQLAQPIA QQIYVEKI
 Sm SloR ELRLLEYDAF AGAYTIEKDG EQLQVTSABA SQIYIEKKAY
 Spn QLQVKQFDGF SNTFTILSND EDLQVNMDIA KQLYVEKIN
 Spy QLQVKQFDGF SNTFTILSND EDLQVNMDIA KQLYVEKIN

CONSENSUS -----

FIGURE 3 cont.

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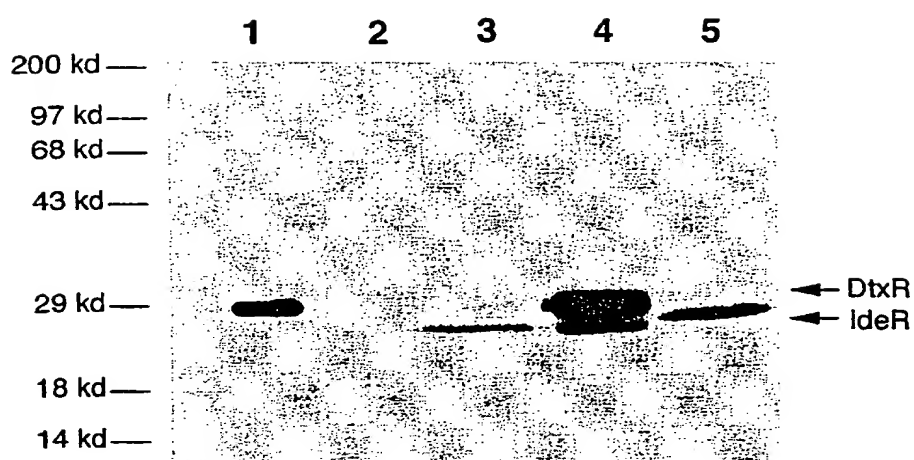


FIGURE 4

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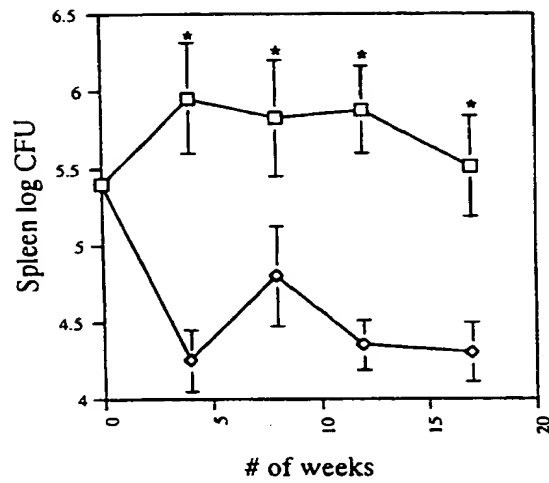


FIGURE 5A

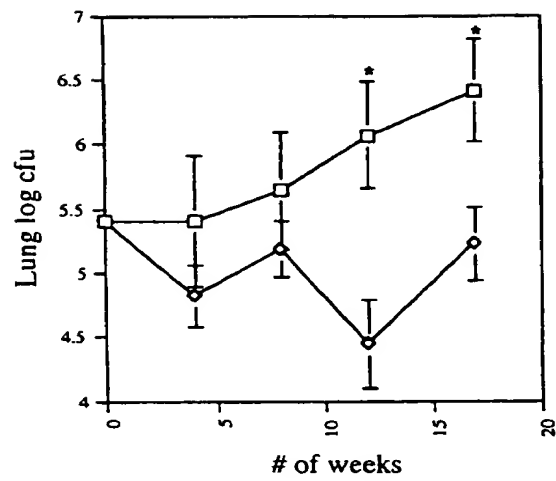


FIGURE 5B

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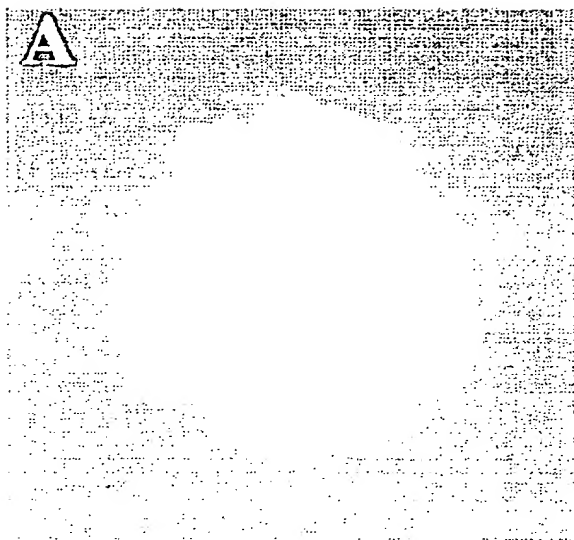


FIGURE 6A

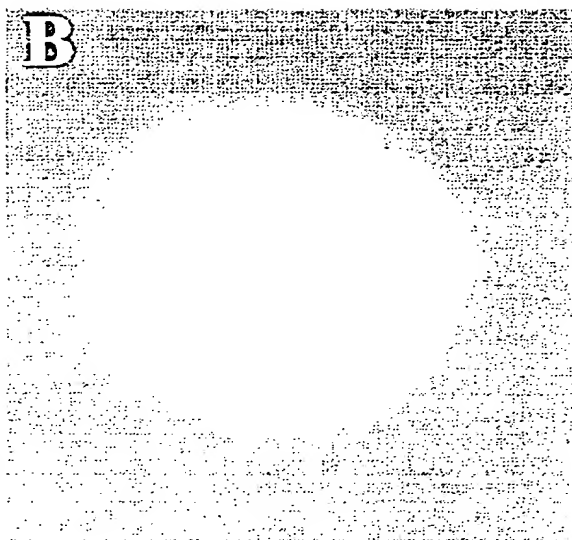


FIGURE 6B

G	T	A	G	G	T	T	A	G	G	C	T	-	A	A	C	C	T	A	T	Consensus Sequence
T	T	A	G	G	T	T	A	G	G	C	T	-	A	A	C	C	T	A	A	Published Consensus
T	T	A	G	G	A	T	A	G	C	T	T	-	T	A	C	C	T	A	A	<i>tox</i> PO <i>C.diphtheriae</i>
T	T	A	G	G	T	T	A	G	G	C	T	-	C	A	C	C	T	A	A	<i>desA</i> PO <i>S.pilosus</i>
C	C	A	G	G	G	T	A	T	C	T	A	-	A	T	C	C	T	G	T	16S ribosomal RNA
G	C	A	G	G	C	C	A	G	T	G	A	-	A	A	C	C	T	G	T	19 kDa antigen
A	C	A	G	G	T	G	G	T	G	C	T	C	A	A	C	C	A	C	G	<i>htrA</i> homologue
G	A	A	G	G	T	A	A	C	G	T	T	C	A	A	C	C	A	A	T	<i>phoP</i> homologue
G	C	A	G	G	T	G	A	C	C	G	T	C	A	A	C	C	G	A	T	<i>adhB</i> homologue
G	A	A	G	G	T	C	A	A	C	C	A	-	A	A	C	A	A	G	A	<i>narG</i> homologue

FIGURE 7

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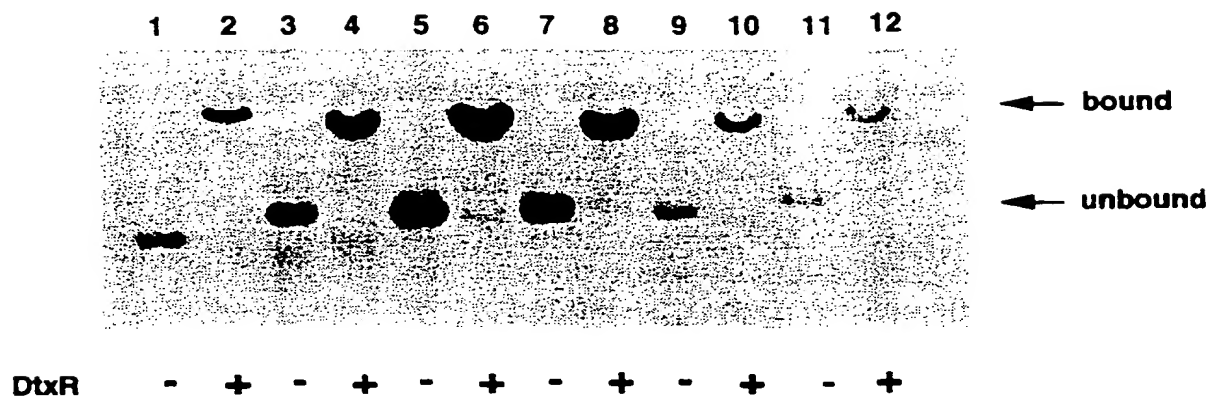


FIGURE 8

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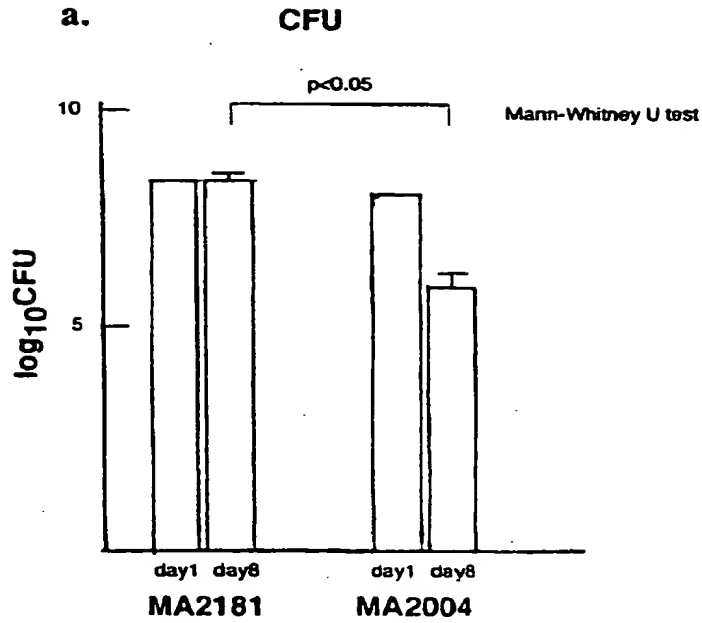


FIGURE 9A

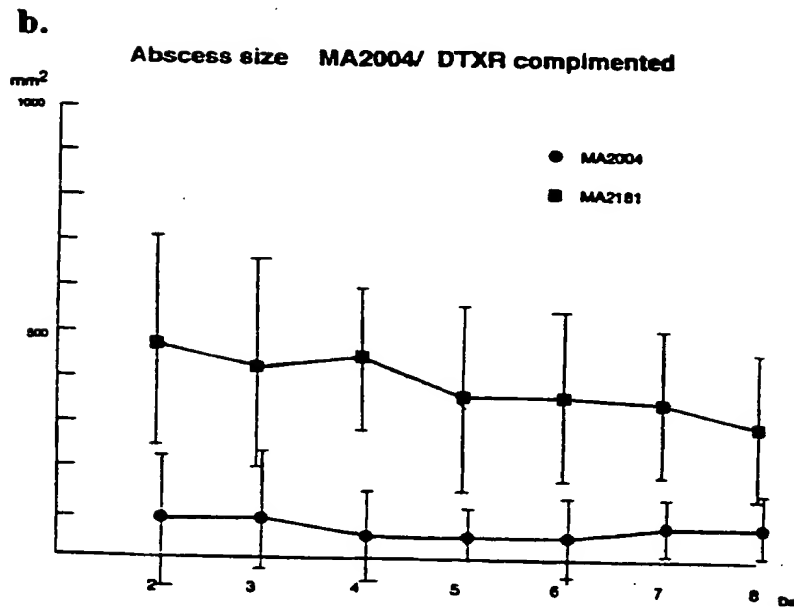


FIGURE 9B